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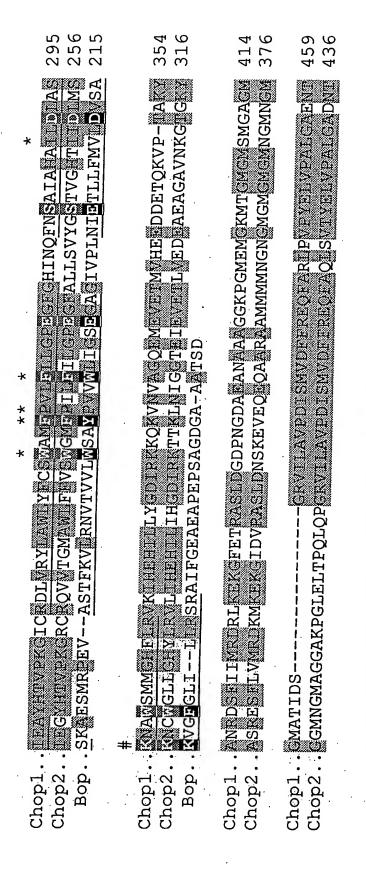
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MiptavegvsqAQiTGRPEWiWLALGTALMGLGTLYFLVKGMGVS
DPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPI
YWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGT
GLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMR
PEVASTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLF
MVLDVSAKVGFGLILLRSRAIFGEAEAPEPSAGDGAAATSD

.}

Fig. 1D

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Chop1..GVEGWIEGPSFGAGINQQALVALINRMQQAKKMGMMG-------GMGMGMGGGMG-N Chop2..nldgwiegpsfgogilpahivalvakmocmrknoomooigmmiggmngmgggmgggmngm Fig. 1D (continued)

LWOOAQSLGGCOFVLMHPEFIRDRSPIGLIPRIKMGGORARAFGWAAIGFWRDIIEGS IVTOAQNLGGVDFVLIBPEFIRPDRSSISRIRGACQRVRAFGWAQLGFWRDIIBSA

Chop1...Com Chop2...A

616 616 G-MAPSINACITGEMER ---ASMGG----AVMCMGMGMGMQPMQQAMP--AMSPM Chop1.. Chop2..

919 667 Chop1..MTQQPS-MMSQPSAMSAGGAMQAMGGVMPSBAP----GGRVGTNPLFGSAPSFLSSQ---Chop2..MnGMSSGVVANVTPSAAGGMGGMMNGGMAAFQSPGMNGGRLGTNFLFNAAPSPLSSQLGA

712 737 ----PGISPONATPPAATAAPAAGGSEATNEQQIMSEINPIN-KIGTK Chop2..EagmgSmggmggmsGmgGmggmggagmarroamg Chop1..-----

Fig. 1D (continued)

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510520530540	
MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWI	40
ESRGTNGAQTASNVLQWLAAGFSILLLMFYAYQTWKSTCG	80
WEEIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLR	120
YAEWLLTCPVILIRLSNLTGLSNDYSRRTMGLLVSDIGTI	160
VWGATSAMATGYVKVIFFCLGLCYGANTFFHAAKAYIEGY	200
HTVPKGRCRQVVTGMAWLFFVSWGMFPILFILGPEGFGVL	240
SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGD	280
IRKTTKLNIGGTEIEVETLVEDEAEAGAVNKGTGK	315

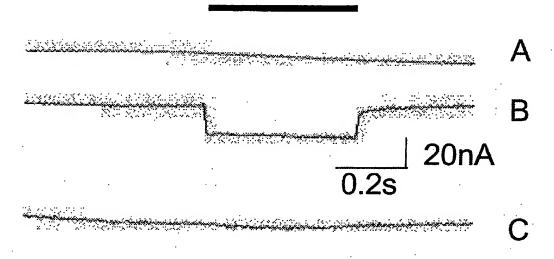
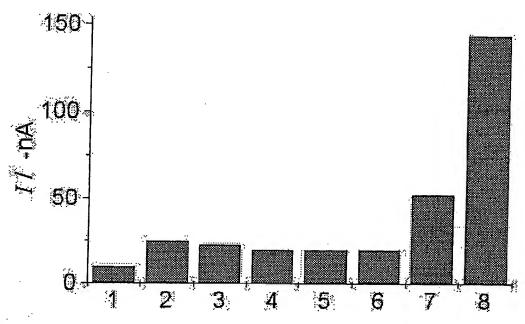


Fig. 2

a



b

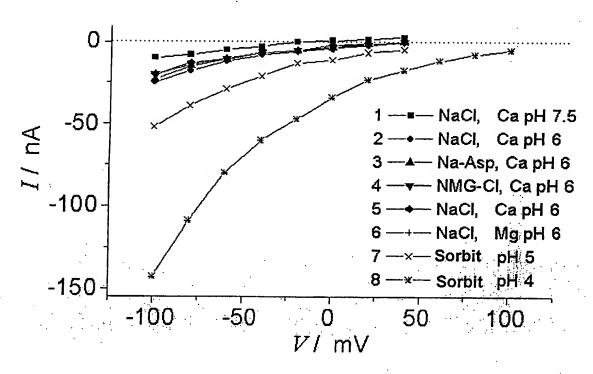
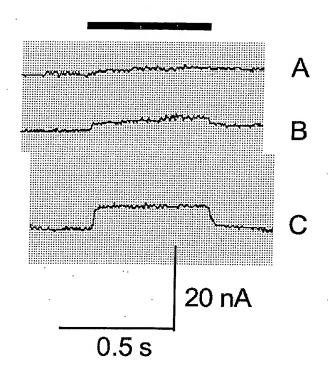


Fig. 3

a



b

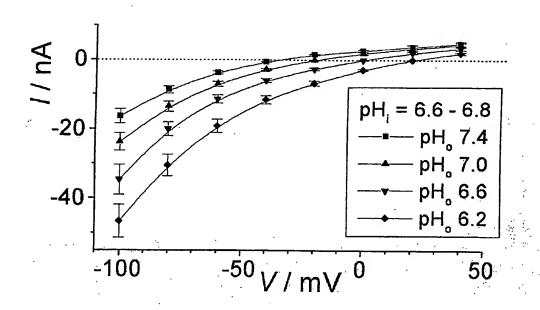
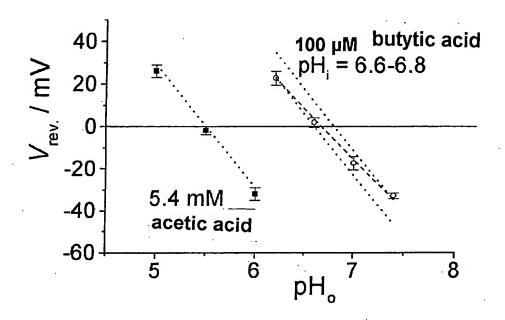


Fig. 4

C



d

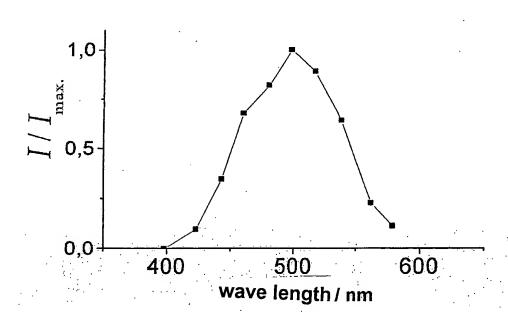


Fig. 4

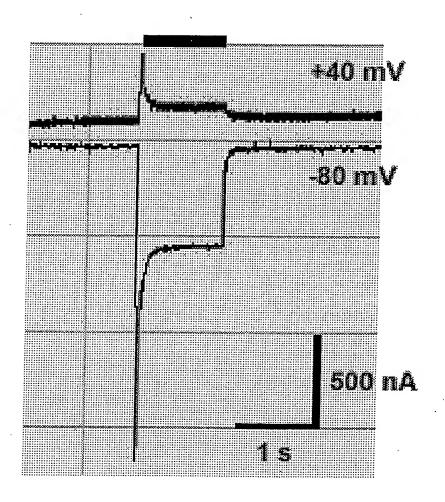


Fig. 5

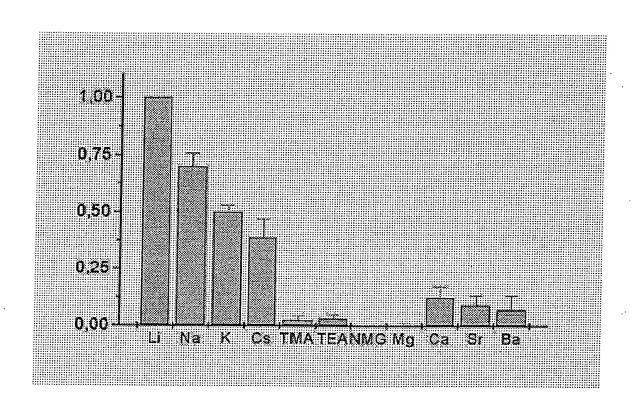


Fig. 6

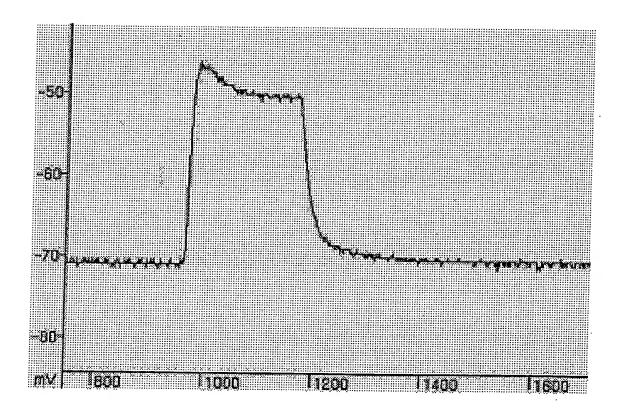


Fig. 7